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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/076,406

DATE: 03/04/2002

TIME: 15:50:57

Input Set : A:\219774US0XCIP.ST25.txt

Output Set: N:\CRF3\03042002\J076406.raw

3 <110> APPLICANT: MOECKEL, Bettina
 4 BATHE, Brigitte
 5 HERMANN, Thomas
 6 PFEFFERLE, Walter
 7 BINDER, Michael
 9 <120> TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
 11 <130> FILE REFERENCE: 219774US0XCIP
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/076,406
 14 <141> CURRENT FILING DATE: 2002-02-19
 16 <150> PRIOR APPLICATION NUMBER: DE 10107229.5
 17 <151> PRIOR FILING DATE: 2001-02-16
 19 <150> PRIOR APPLICATION NUMBER: US 09/887052
 20 <151> PRIOR FILING DATE: 2001-06-25
 22 <160> NUMBER OF SEQ ID NOS: 12
 24 <170> SOFTWARE: PatentIn version 3.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 5099
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Corynebacterium glutamicum
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (702)..(4196)
 34 <223> OTHER INFORMATION:
 37 <400> SEQUENCE: 1

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42	tcgacgcctc	cctcgacgat	gcagctgtct	ctaagctggt	tgacacaggcc	gaaagcatcc	180	
44	ctgatggaga	tgtgagcaaa	atcgcaaata	ccgtagggtat	tgtgatcggg	gcggtattgg	240	
46	ctctcgtggg	cctggccggg	tgttttgggg	cgtttgggaa	gaaacgtcga	gaagcttaac	300	
48	ctgctgttca	aatagatttt	ccctgtttcg	aattgcggaa	accccggtt	tgtttgctag	360	
50	ggtgcctcgt	agaaggggtc	aagaagattt	ctgggaaacg	cgcccgtgcg	gttggttget	420	
52	aatagcacgc	ggagcaccag	atgaaaaatc	tcccctttac	tttcgcgcgc	gattggtata	480	
54	ctctgagtcg	ttgcgttggg	attcgtgact	ctttttcggt	cctgtagcgc	caagaccttg	540	
56	atcaaggtgg	tttaaaaaaa	ccgatttgac	aaggtcattc	agtgcctatc	ggagtcgttc	600	
58	aggggggatc	ggttcctcag	cagaccaatt	gctcaaaaat	accagcgggtg	ttgatctgca	660	
60	cttaatggcc	ttgaccagcc	aggtgcaatt	acccgcgtga	g	gtg ctg gaa gga ccc	716	
61					Val	Leu Glu Gly Pro		
62					1	5		
64	atc ttg	gca gtc	tcc cgc	cag acc	aag tca	gtc gtc	gat att ccc ggt	764
65	Ile Leu	Ala Val	Ser Arg	Gln Thr	Lys Ser	Val Val	Asp Ile Pro Gly	
66		10		15		20		
68	gca ccg	cag cgt	tat tct	ttc gcg	aag gtg	tcc gca	ccc att gag gtg	812
69	Ala Pro	Gln Arg	Tyr Ser	Phe Ala	Lys Val	Ser Ala	Pro Ile Glu Val	

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70	25	30	35	
72	ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt	860		
73	Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly			
74	40 45 50			
76	acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc	908		
77	Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala			
78	55 60 65			
80	cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc	956		
81	Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile			
82	70 75 80 85			
84	cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc	1004		
85	Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe			
86	90 95 100			
88	gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac	1052		
89	Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn			
90	105 110 115			
92	tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc	1100		
93	Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr			
94	120 125 130			
96	ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg	1148		
97	Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met			
98	135 140 145			
100	acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc	1196		
101	Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val			
102	150 155 160 165			
104	agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat	1244		
105	Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp			
106	170 175 180			
108	aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt	1292		
109	Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg			
110	185 190 195			
112	ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt	1340		
113	Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val			
114	200 205 210			
116	cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct	1388		
117	Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala			
118	215 220 225			
120	ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa	1436		
121	Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu			
122	230 235 240 245			
124	atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag	1484		
125	Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu			
126	250 255 260			
128	gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc	1532		
129	Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr			
130	265 270 275			
132	cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag	1580		
133	Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys			
134	280 285 290			

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136	cgc	tac	gac	ctg	gct	cgc	ggt	ggt	cgt	tac	aag	atc	aac	cgc	aag	ctc	1628
137	Arg	Tyr	Asp	Leu	Ala	Arg	Val	Gly	Arg	Tyr	Lys	Ile	Asn	Arg	Lys	Leu	
138		295					300				305						
140	ggc	ctt	ggt	ggc	gac	cac	gat	ggt	ttg	atg	act	ctt	act	gaa	gag	gac	1676
141	Gly	Leu	Gly	Gly	Asp	His	Asp	Gly	Leu	Met	Thr	Leu	Thr	Glu	Glu	Asp	
142	310					315					320					325	
144	atc	gca	acc	acc	atc	gag	tac	ctg	gtg	cgt	ctg	cac	gca	ggt	gag	cgc	1724
145	Ile	Ala	Thr	Thr	Ile	Glu	Tyr	Leu	Val	Arg	Leu	His	Ala	Gly	Glu	Arg	
146					330					335					340		
148	gtc	atg	act	tct	cca	aat	ggt	gaa	gag	atc	cca	gtc	gag	acc	gat	gac	1772
149	Val	Met	Thr	Ser	Pro	Asn	Gly	Glu	Glu	Ile	Pro	Val	Glu	Thr	Asp	Asp	
150				345					350					355			
152	atc	gac	cac	ttt	ggt	aac	cgt	cgt	ctg	cgt	acc	ggt	ggc	gaa	ctg	atc	1820
153	Ile	Asp	His	Phe	Gly	Asn	Arg	Arg	Leu	Arg	Thr	Val	Gly	Glu	Leu	Ile	
154			360					365					370				
156	cag	aac	cag	gtc	cgt	gtc	ggc	ctg	tcc	cgc	atg	gag	cgc	ggt	ggt	cgt	1868
157	Gln	Asn	Gln	Val	Arg	Val	Gly	Leu	Ser	Arg	Met	Glu	Arg	Val	Val	Arg	
158		375					380					385					
160	gag	cgt	atg	acc	acc	cag	gat	gcg	gag	tcc	att	act	cct	act	tcc	ttg	1916
161	Glu	Arg	Met	Thr	Thr	Gln	Asp	Ala	Glu	Ser	Ile	Thr	Pro	Thr	Ser	Leu	
162	390					395					400					405	
164	atc	aac	ggt	cgt	cct	gtc	tct	gca	gct	atc	cgt	gag	ttc	ttc	gga	act	1964
165	Ile	Asn	Val	Arg	Pro	Val	Ser	Ala	Ala	Ile	Arg	Glu	Phe	Phe	Gly	Thr	
166				410						415					420		
168	tcc	cag	ctg	tct	cag	ttc	atg	gac	cag	aac	aac	tcc	ctg	tct	ggt	ttg	2012
169	Ser	Gln	Leu	Ser	Gln	Phe	Met	Asp	Gln	Asn	Asn	Ser	Leu	Ser	Gly	Leu	
170			425						430						435		
172	act	cac	aag	cgt	cgt	ctg	tcg	gct	ctg	ggc	ccg	ggt	ggt	ctg	tcc	cgt	2060
173	Thr	His	Lys	Arg	Arg	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Gly	Leu	Ser	Arg	
174			440					445						450			
176	gag	cgc	gcc	ggc	atc	gag	ggt	cga	gac	ggt	cac	cca	tct	cac	tac	ggc	2108
177	Glu	Arg	Ala	Gly	Ile	Glu	Val	Arg	Asp	Val	His	Pro	Ser	His	Tyr	Gly	
178		455				460						465					
180	cgt	atg	tgc	cca	att	gag	act	ccg	gaa	ggt	cca	aac	att	ggc	ctg	atc	2156
181	Arg	Met	Cys	Pro	Ile	Glu	Thr	Pro	Glu	Gly	Pro	Asn	Ile	Gly	Leu	Ile	
182	470					475					480					485	
184	ggt	tcc	ttg	gct	tcc	tat	gct	cga	gtg	aac	cca	ttc	ggt	ttc	att	gag	2204
185	Gly	Ser	Leu	Ala	Ser	Tyr	Ala	Arg	Val	Asn	Pro	Phe	Gly	Phe	Ile	Glu	
186				490						495					500		
188	acc	cca	tac	cgt	cgc	atc	atc	gac	ggc	aag	ctg	acc	gac	cag	att	gac	2252
189	Thr	Pro	Tyr	Arg	Arg	Ile	Ile	Asp	Gly	Lys	Leu	Thr	Asp	Gln	Ile	Asp	
190				505					510						515		
192	tac	ctt	acc	gct	gat	gag	gaa	gac	cgc	ttc	ggt	ggt	gcg	cag	gca	aac	2300
193	Tyr	Leu	Thr	Ala	Asp	Glu	Glu	Asp	Arg	Phe	Val	Val	Ala	Gln	Ala	Asn	
194			520					525					530				
196	acg	cac	tac	gac	gaa	gag	ggc	aac	atc	acc	gat	gag	acc	gtc	act	ggt	2348
197	Thr	His	Tyr	Asp	Glu	Glu	Gly	Asn	Ile	Thr	Asp	Glu	Thr	Val	Thr	Val	
198		535					540					545					
200	cgt	ctg	aag	gac	ggc	gac	atc	gcc	atg	ggt	ggc	cgc	aac	gcg	ggt	gat	2396

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201	Arg	Leu	Lys	Asp	Gly	Asp	Ile	Ala	Met	Val	Gly	Arg	Asn	Ala	Val	Asp	
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204	tac	atg	gac	gtt	tcc	cct	cgt	cag	atg	gtt	tct	gtt	ggt	acc	gcg	atg	2444
205	Tyr	Met	Asp	Val	Ser	Pro	Arg	Gln	Met	Val	Ser	Val	Gly	Thr	Ala	Met	
206					570					575						580	
208	att	cca	ttc	ctg	gag	cac	gac	gat	gct	aac	cgt	gca	ctg	atg	ggc	gcg	2492
209	Ile	Pro	Phe	Leu	Glu	His	Asp	Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Ala	
210				585					590					595			
212	aac	atg	cag	aag	cag	gct	gtg	cca	ctg	att	cgt	gcc	gag	gct	cct	ttc	2540
213	Asn	Met	Gln	Lys	Gln	Ala	Val	Pro	Leu	Ile	Arg	Ala	Glu	Ala	Pro	Phe	
214			600					605						610			
216	gtg	ggc	acc	ggt	atg	gag	cag	cgc	gca	gca	tac	gac	gcc	ggc	gac	ctg	2588
217	Val	Gly	Thr	Gly	Met	Glu	Gln	Arg	Ala	Ala	Tyr	Asp	Ala	Gly	Asp	Leu	
218		615					620				625						
220	gtt	att	acc	cca	gtc	gca	ggt	gtg	gtg	gaa	aac	gtt	tca	gct	gac	ttc	2636
221	Val	Ile	Thr	Pro	Val	Ala	Gly	Val	Val	Glu	Asn	Val	Ser	Ala	Asp	Phe	
222	630					635				640						645	
224	atc	acc	atc	atg	gct	gat	gac	ggc	aag	cgc	gaa	acc	tac	ctg	ctg	cgt	2684
225	Ile	Thr	Ile	Met	Ala	Asp	Asp	Gly	Lys	Arg	Glu	Thr	Tyr	Leu	Leu	Arg	
226				650					655						660		
228	aag	ttc	cag	cgc	acc	aac	cag	ggc	acc	agc	tac	aac	cag	aag	cct	ttg	2732
229	Lys	Phe	Gln	Arg	Thr	Asn	Gln	Gly	Thr	Ser	Tyr	Asn	Gln	Lys	Pro	Leu	
230			665					670						675			
232	gtt	aac	ttg	ggc	gag	cgc	gtt	gaa	gct	ggc	cag	gtt	att	gct	gat	ggt	2780
233	Val	Asn	Leu	Gly	Glu	Arg	Val	Glu	Ala	Gly	Gln	Val	Ile	Ala	Asp	Gly	
234		680					685							690			
236	cca	ggt	acc	ttc	aat	ggt	gaa	atg	tcc	ctt	ggc	cgt	aac	ctt	ctg	gtt	2828
237	Pro	Gly	Thr	Phe	Asn	Gly	Glu	Met	Ser	Leu	Gly	Arg	Asn	Leu	Leu	Val	
238		695				700					705						
240	gcg	ttc	atg	cct	tgg	gaa	ggc	cac	aac	tac	gag	gat	gcg	atc	atc	ctc	2876
241	Ala	Phe	Met	Pro	Trp	Glu	Gly	His	Asn	Tyr	Glu	Asp	Ala	Ile	Ile	Leu	
242	710					715					720					725	
244	aac	cag	aac	atc	gtt	gag	cag	gac	atc	ttg	acc	tcg	atc	cac	atc	gag	2924
245	Asn	Gln	Asn	Ile	Val	Glu	Gln	Asp	Ile	Leu	Thr	Ser	Ile	His	Ile	Glu	
246				730					735						740		
248	gag	cac	gag	atc	gat	gcc	cgc	gac	act	aag	ctt	ggc	gcc	gaa	gaa	atc	2972
249	Glu	His	Glu	Ile	Asp	Ala	Arg	Asp	Thr	Lys	Leu	Gly	Ala	Glu	Glu	Ile	
250			745					750						755			
252	acc	cgc	gac	atc	cct	aat	gtg	tct	gaa	gaa	gtc	ctc	aag	gac	ctc	gac	3020
253	Thr	Arg	Asp	Ile	Pro	Asn	Val	Ser	Glu	Glu	Val	Leu	Lys	Asp	Leu	Asp	
254			760					765						770			
256	gac	cgc	ggt	att	gtc	cgc	atc	ggt	gct	gat	gtt	cgt	gac	ggc	gac	atc	3068
257	Asp	Arg	Gly	Ile	Val	Arg	Ile	Gly	Ala	Asp	Val	Arg	Asp	Gly	Asp	Ile	
258		775					780							785			
260	ctg	gtc	ggt	aag	gtc	acc	cct	aag	ggc	gag	acc	gag	ctc	acc	ccg	gaa	3116
261	Leu	Val	Gly	Lys	Val	Thr	Pro	Lys	Gly	Glu	Thr	Glu	Leu	Thr	Pro	Glu	
262	790					795					800					805	
264	gag	cgc	ttg	ctg	cgc	gca	atc	ttc	ggt	gag	aag	gcc	cgc	gaa	gtt	cgc	3164
265	Glu	Arg	Leu	Leu	Arg	Ala	Ile	Phe	Gly	Glu	Lys	Ala	Arg	Glu	Val	Arg	

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268	gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc						3212
269	Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly						
270		825		830		835	
272	gtg cgt cac ttc tcc cgc gag gac gac gat ctg gct cct ggc gtc						3260
273	Val Arg His Phe Ser Arg Glu Asp Asp Asp Leu Ala Pro Gly Val						
274		840		845		850	
276	aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac						3308
277	Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp						
278		855		860		865	
280	ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa						3356
281	Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys						
282	870		875		880		885
284	att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt						3404
285	Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val						
286		890		895		900	
288	gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt						3452
289	Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly						
290		905		910		915	
292	cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc						3500
293	Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser						
294		920		925		930	
296	gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct						3548
297	Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro						
298		935		940		945	
300	gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg						3596
301	Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val						
302	950		955		960		965
304	ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca						3644
305	Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser						
306		970		975		980	
308	cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca						3692
309	Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala						
310		985		990		995	
312	acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt						3737
313	Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val						
314		1000		1005		1010	
316	tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac						3782
317	Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp						
318		1015		1020		1025	
320	gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc						3827
321	Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr						
322		1030		1035		1040	
324	cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc						3872
325	Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe						
326		1045		1050		1055	
328	ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac						3917
329	Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr						
330		1060		1065		1070	

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number